Reviewer’s report

Title: Planning for the next influenza H1N1 season: a modelling study

Version: 2 Date: 4 July 2010

Reviewer: Junling Ma

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In the manuscript "Planning for the next influenza H1N1 season: a modelling study" by Carrat et al, the authors use a sophisticated individual based model to explain the observed epidemic curve for for influenza like illness (ILI) during the 2009 pH1N1 influenza pandemic using French national surveillance data. The research questions are the attack rates and pre-exposure cross-resistance levels in different age groups, and the possibility of a second season caused by the mutants of the pandemic strain depending on different levels of cross-resistance to the mutant strain. These questions are all important in preparing for a possible second season of pH1N1 influenza.

Major Compulsory Revisions

However, the estimated effective reproduction number presented in this manuscript is 1.05, which is substantially lower than other estimations of the pandemic in Mexico and other countries (ranging from 1.6-2, see, for example, Fraser et al., (2009, Science), Nishiura et al, (2009, Euro Surveill), Nishiura et al, (2009, J. NZ Med. Assoc.)) and more close to seasonal influenza. Note that in all these published estimations, the population is treated as fully susceptible, so in fact they estimated the effective reproduction number if pre-exposure resistance exists.

The authors need justify this discrepancy. Clarify a few points below may help us justify the results. Some of these information may be provided in supplementary material.

1. If the effective reproduction number is so low, which is comparable with that of seasonal influenza, how does the French pandemic curve (exponential growth rate and final size) compare with those of other seasonal influenza?

2. Is the data used in this research the same as in Fuhrman et al, (2010, Eurosursveillance)? Does it suffer the same change in surveillance as shown in the mentioned paper?

3. Clarify the model used for fitting. I suspect it is an epidemic model on a contact network, with constant per-link transmission rate and degree distributions. If so, does it consider network clustering? As including clustering may greatly change the outcome of an epidemic.

4. How many parameters are estimated? In the manuscript two are mentioned,
namely, the pre-exposure resistance levels in younger and elder adults. But how are transmission rates and initial conditions determined?

5. Specify the statistical method used in fitting. How are confidence intervals computed?

6. The authors seem to use nonlinear least square regression. If it is true, this method treats the error at each observation independently identically distributed. On the other hand, in an epidemic, the variance of error grows with the mean. So the least square method tends to bias towards the peak and final size, and generally yields unreliable approximation of the exponential growth phase. The exponential growth phase is more dependent on R0. In contrary, the peak and final size are not good indicators of R0 as changing the reporting ratio may change the estimation significantly. The authors should use more appropriate statistical methods such as minimum chi-square or maximum likelihood methods.

Minor Essential Revisions

1. State that the surveillance data is aggregated weekly.

2. In figure 2, plot the average of the simulated curves, which is used to approximate the observed epidemic curve (blue) in fitting.

Level of interest: An article of importance in its field

Quality of written English: Acceptable

Statistical review: Yes, and I have assessed the statistics in my report.